# STIC Biotechnology Systems Branch

## RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: *10/527,257*

Source: *PCT/10*

Date Processed by STIC: *1/11/06*

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 4.2.2 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

**http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm**

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio **(<http://www.uspto.gov/ebc/efs/downloads/documents.htm>** , **EFS Submission User Manual** - ePAVE)
2. **U.S. Postal Service:** Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. **Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):** U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/24/05

# Raw Sequence Listing Error Summary

| ERROR DETECTED | SUGGESTED CORRECTION | SERIAL NUMBER: _10/527,257_ |
|---|---|---|

**ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE**

**1_____Wrapped Nucleics**
**Wrapped Aminos**
The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor **after** creating it. Please adjust your right margin to .3; this will prevent "wrapping."

**2_____Invalid Line Length**
The rules require that a line **not exceed** 72 characters in length. This includes white spaces.

**3_____Misaligned Amino**
**Numbering**
The numbering under each 5th amino acid is misaligned. Do **not** use tab codes between numbers; use **space characters**, instead.

**4_____Non-ASCII**
The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. **Please ensure your subsequent submission is saved in ASCII text.**

**5_____Variable Length**
Sequence(s)_____contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the **maximum** number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

**6_____PatentIn 2.0**
**"bug"**
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**

**7_____Skipped Sequences**
**(OLD RULES)**
Sequence(s) _____ missing. If intentional, please insert the following lines for **each** skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)         SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.

**8_____Skipped Sequences**
**(NEW RULES)**
Sequence(s) _____ missing. If **intentional**, please insert the following lines for **each** skipped sequence.
<210> sequence id number
<400> sequence id number
000

**9_____Use of n's or Xaa's**
**(NEW RULES)**
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of **n** or **Xaa**, and which residue **n** or **Xaa** represents.

**10_____Invalid <213>**
**Response**
Per 1.823 of Sequence Rules, the only **valid** <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or is Artificial Sequence

**11_____Use of <220>**
Sequence(s)_____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of Sequence Rules)

**12_____PatentIn 2.0**
**"bug"**
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

**13_____Misuse of n/Xaa**
"n" can **only** represent a single <u>nucleotide</u>; "Xaa" can **only** represent a single <u>amino acid</u>

AMC – Biotechnology Systems Branch – 09/09/2003

RAW SEQUENCE LISTING                    DATE: 01/11/2006
PATENT APPLICATION:  US/10/527,257     TIME: 14:12:07

        Input Set : A:\186353 US - Sequence Listing 10 527257.txt
        Output Set: N:\CRF4\01112006\J527257.raw

```
 3 <110> APPLICANT: Wu, Jun
 4         Luo, Ying
 6 <120> TITLE OF INVENTION: TUMOR TAG AND THE USE THEREOF
 8 <130> FILE REFERENCE: 024455
C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/527,257
C--> 10 <141> CURRENT FILING DATE: 2005-03-09
10 <160> NUMBER OF SEQ ID NOS: 9
12 <170> SOFTWARE: PatentIn version 3.1
14 <210> SEQ ID NO: 1
15 <211> LENGTH: 720
16 <212> TYPE: DNA
17 <213> ORGANISM: Homo sapiens
19 <220> FEATURE:
20 <221> NAME/KEY: CDS
21 <222> LOCATION: (1)..(639)
22 <223> OTHER INFORMATION:
W--> 25 <400> 1
26 atg gca gcg gcc gcc agc ccc gcg ttc ctt cta cgc ctc ccg ctt ctg    48
27 Met Ala Ala Ala Ala Ser Pro Ala Phe Leu Leu Arg Leu Pro Leu Leu
28 1               5                   10                  15
30 ctc ctg ctg tcc agc tgg tgc agg acc ggg ctg gcc gac cct cac tct    96
31 Leu Leu Leu Ser Ser Trp Cys Arg Thr Gly Leu Ala Asp Pro His Ser
32             20                  25                  30
34 ctt tgc tat gac atc acc gtc atc cct aag ttc aga cct gga cca cgg   144
35 Leu Cys Tyr Asp Ile Thr Val Ile Pro Lys Phe Arg Pro Gly Pro Arg
36         35                  40                  45
38 tgg tgt gcg gtt caa ggc cag gtg gat gaa aag act ttt ctt cac tat   192
39 Trp Cys Ala Val Gln Gly Gln Val Asp Glu Lys Thr Phe Leu His Tyr
40     50                  55                  60
42 gac tgt ggc agc aag aca gtc aca ccc gtc agt ccc ctg ggg aag aaa   240
43 Asp Cys Gly Ser Lys Thr Val Thr Pro Val Ser Pro Leu Gly Lys Lys
44 65                  70                  75                  80
46 cta aat gtc aca acg gcc tgg aaa gca cag aac cca gta ctg aga gag   288
47 Leu Asn Val Thr Thr Ala Trp Lys Ala Gln Asn Pro Val Leu Arg Glu
48                  85                  90                  95
50 gtg gtg gac ata ctt aca gag caa ctg ctt gac att cag ctg gag aat   336
51 Val Val Asp Ile Leu Thr Glu Gln Leu Leu Asp Ile Gln Leu Glu Asn
52                  100                 105                 110
54 tac ata ccc aag gaa ccc ctc acc ctg cag gcc agg atg tct tgt gag   384
55 Tyr Ile Pro Lys Glu Pro Leu Thr Leu Gln Ala Arg Met Ser Cys Glu
56             115                 120                 125
58 cag aaa gcc gaa gga cac ggc agt gga tct tgg cag ctc agt ttc gat   432
59 Gln Lys Ala Glu Gly His Gly Ser Gly Ser Trp Gln Leu Ser Phe Asp
```

Does Not Comply
Corrected Diskette Needed

P.3

RAW SEQUENCE LISTING                    DATE: 01/11/2006
PATENT APPLICATION:  US/10/527,257      TIME: 14:12:07

Input Set : A:\186353 US - Sequence Listing 10 527257.txt
Output Set: N:\CRF4\01112006\J527257.raw

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60      130                   135                   140
62 gga cag atc ttc ctc ctc ttt gac tca gaa aac aga atg tgg aca acg      480
63 Gly Gln Ile Phe Leu Leu Phe Asp Ser Glu Asn Arg Met Trp Thr Thr
64 145                   150                   155                   160
66 gtt cat cct gga gcc aga aag atg aaa gaa aag tgg gag aat gac aag      528
67 Val His Pro Gly Ala Arg Lys Met Lys Glu Lys Trp Glu Asn Asp Lys
68                   165                   170                   175
70 gat atg acc atg tcc ttc cat tac atc tca atg gga gac tgc aca gga      576
71 Asp Met Thr Met Ser Phe His Tyr Ile Ser Met Gly Asp Cys Thr Gly
72                   180                   185                   190
74 tgg ctt gag gac ttc ttg atg ggc atg gac agc acc ctg gag cca agt      624
75 Trp Leu Glu Asp Phe Leu Met Gly Met Asp Ser Thr Leu Glu Pro Ser
76            195                   200                   205
78 gca gga ggc aca gtc tgacccaaag ccatggccac caccctcagt ccctgcagcc     679
79 Ala Gly Gly Thr Val
80      210
82 tcctcctcat cctcccctgc ttcatcctcc ctggcatctg a                       720
85 <210> SEQ ID NO: 2
86 <211> LENGTH: 213
87 <212> TYPE: PRT
88 <213> ORGANISM: Homo sapiens
90 <400> SEQUENCE: 2
92 Met Ala Ala Ala Ala Ser Pro Ala Phe Leu Leu Arg Leu Pro Leu Leu
93 1                   5                   10                  15
96 Leu Leu Leu Ser Ser Trp Cys Arg Thr Gly Leu Ala Asp Pro His Ser
97            20                  25                  30
100 Leu Cys Tyr Asp Ile Thr Val Ile Pro Lys Phe Arg Pro Gly Pro Arg
101          35                  40                  45
104 Trp Cys Ala Val Gln Gly Gln Val Asp Glu Lys Thr Phe Leu His Tyr
105       50                  55                  60
108 Asp Cys Gly Ser Lys Thr Val Thr Pro Val Ser Pro Leu Gly Lys Lys
109 65                  70                  75                  80
112 Leu Asn Val Thr Thr Ala Trp Lys Ala Gln Asn Pro Val Leu Arg Glu
113                  85                  90                  95
116 Val Val Asp Ile Leu Thr Glu Gln Leu Leu Asp Ile Gln Leu Glu Asn
117          100                 105                 110
120 Tyr Ile Pro Lys Glu Pro Leu Thr Leu Gln Ala Arg Met Ser Cys Glu
121          115                 120                 125
124 Gln Lys Ala Glu Gly His Gly Ser Gly Ser Trp Gln Leu Ser Phe Asp
125       130                 135                 140
128 Gly Gln Ile Phe Leu Leu Phe Asp Ser Glu Asn Arg Met Trp Thr Thr
129 145                 150                 155                 160
132 Val His Pro Gly Ala Arg Lys Met Lys Glu Lys Trp Glu Asn Asp Lys
133                  165                 170                 175
136 Asp Met Thr Met Ser Phe His Tyr Ile Ser Met Gly Asp Cys Thr Gly
137                  180                 185                 190
140 Trp Leu Glu Asp Phe Leu Met Gly Met Asp Ser Thr Leu Glu Pro Ser
141          195                 200                 205
144 Ala Gly Gly Thr Val
```

```
145      210
148 <210> SEQ ID NO: 3
149 <211> LENGTH: 29
150 <212> TYPE: DNA
151 <213> ORGANISM: primer         invalid response- see item 10 on Error
153 <400> SEQUENCE: 3                                          Summary
154 cggaattcat ggcagcggcc gccagcccc                      29   Sheet
157 <210> SEQ ID NO: 4
158 <211> LENGTH: 30
159 <212> TYPE: DNA
160 <213> ORGANISM: primer
162 <400> SEQUENCE: 4
163 gccaagcttg atgccaggga ggatgaagca                     30
166 <210> SEQ ID NO: 5
167 <211> LENGTH: 34
168 <212> TYPE: DNA
169 <213> ORGANISM: primer
171 <400> SEQUENCE: 5
172 ccggaattcg accctcactc tctttgctat gaca               34
175 <210> SEQ ID NO: 6
176 <211> LENGTH: 30
177 <212> TYPE: DNA
178 <213> ORGANISM: primer
180 <400> SEQUENCE: 6
181 gccaagcttg atgccaggga ggatgaagca                     30
184 <210> SEQ ID NO: 7
185 <211> LENGTH: 21
186 <212> TYPE: DNA
187 <213> ORGANISM: primer
189 <400> SEQUENCE: 7
190 atggcagcgg ccgccagccc c                              21
193 <210> SEQ ID NO: 8
194 <211> LENGTH: 24
195 <212> TYPE: DNA
196 <213> ORGANISM: primer
198 <400> SEQUENCE: 8
199 tcagatgcca gggaggatga agca                           24
202 <210> SEQ ID NO: 9
203 <211> LENGTH: 742
204 <212> TYPE: DNA
205 <213> ORGANISM: Homo sapiens
207 <400> SEQUENCE: 9
208 atggcagcgg ccgccagccc cgcgttcctt ctacgcctcc cgcttctgct cctgctgtcc    60
210 agctggtgca ggaccgggct ggccgaccct cactctcttt gctatgacat caccgtcatc   120
212 cctaagttca gacctggacc acggtggtgt gcggttcaag gccaggtgga tgaaaagact   180
214 tttcttcact atgactgtgg cagcaagaca gtcacacccg tcagtcccct ggggaagaaa   240
216 ctaaatgtca caacggcctg gaaagcacag aacccagtac tgagagaggt ggtggacata   300
218 cttacagagc aactgcttga cattcagctg gagaattaca tacccaagga acccctcacc   360
220 ctgcaggcca ggatgtcttg tgagcagaaa gccgaaggac acggcagtgg atcttggcag   420
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222 ctcagtttcg atggacagat cttcctcctc tttgactcag aaaacagaat gtggacaacg    480
224 gttcatcctg gagccagaaa gatgaaagaa aagtgggaga atgacaagga tatgaccatg    540
226 tccttccatt acatctcaat gggagactgc acaggatggc ttgaggactt cttgatgggc    600
228 atggacagca ccctggagcc aagtgcagga gcaccaccca ccatgtcctc aggcacagcc    660
230 caacccaggg ccacggccac caccctcatc ctttgctgcc tcctcatcat gtgtctcctc    720
232 atatgctcca ggcacagtct ga                                             742
```

**VERIFICATION SUMMARY**
PATENT APPLICATION:   **US/10/527,257**

DATE: 01/11/2006
TIME: 14:12:08

Input Set : **A:\186353 US - Sequence Listing 10 527257.txt**
Output Set: **N:\CRF4\01112006\J527257.raw**

L:10 M:270 C: Current Application Number differs, Replaced Current Application No
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:25 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:22